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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/019,048	12/27/2001	Ernst Heinz	0093/000032	5170

26474 7590 06/26/2006

NOVAK DRUCE DELUCA & QUIGG, LLP
1300 EYE STREET NW
SUITE 400 EAST TOWER
WASHINGTON, DC 20005

EXAMINER

GUZO, DAVID

ART UNIT PAPER NUMBER

1636

DATE MAILED: 06/26/2006

Please find below and/or attached an Office communication concerning this application or proceeding.



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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER
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3

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

— SEE ATTACHMENT AND
NOTICE TO COMPLY WITH
THE SEQUENCE RULES —

Notice to Comply	Application No. 10/019,048	Applicant(s) Heinz et al.	
	Examiner David Guzo	Art Unit 1636	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216 or (703) 308-2923

For CRF Submission Help, call (703) 308-4212 or 308-2923

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Attachment

The reply filed on 4/5/06 is not fully responsive to the prior Office Action because of the following omission(s) or matter(s): The Sequence Listing filed 4/5/06 contains errors and cannot be entered (See attached Raw Sequence Listing Error Report). See 37 CFR 1.111. Since the above-mentioned reply appears to be *bona fide*, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David Guzo, Ph.D., whose telephone number is (571) 272-0767. The examiner can normally be reached on Monday-Thursday from 8:00 AM to 5:30 PM. The examiner can also be reached on alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Irem Yucel, Ph.D., can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David Guzo
June 14, 2006


DAVID GUZO
PRIMARY EXAMINER

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,048A
Source: FWK
Date Processed by STIC: 4/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/019,048A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 c Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

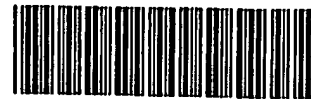
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

*Please consult Sequence Rules
for valid format*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006

TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

C--> 3 <140> CURRENT APPLICATION NUMBER: US/10/019,048A
E--> 0 <160> NUMBER OF SEQ ID NOS:
3 <170> SOFTWARE: PatentIn Vers. 3.3

see p. 5

ERRORED SEQUENCES

5 <210> SEQ ID NO: 1
6 <211> LENGTH: 2012
7 <212> TYPE: DNA
8 <213> ORGANISM: Physcomitrella patens
10 <220> FEATURE:
11 <221> NAME/KEY: CDS
12 <222> LOCATION: (319)..(1896)

**Does Not Comply
Corrected Diskette Needed**

OK

see p. 3

14 <400> SEQUENCE: 1
15 ccgagtcgcg gatcagccat cgcccgcgcc gggccgcctg cattgtgttg gacgggtgtg 60
17 gagaggagg cagatgcgcg ggcgttggtg gactcgtcat ccgaggatct actgcggcaa 120
19 tacctccggg ttttgagcg ggcaaaactct gttgcggctc ggaaggctat aggttcggca 180
21 ggagactgtt gattttatgt cgggggcatt gccattgttg agagcggggg agactcagga 240
23 tctgtgagtg tgcgtgcagc gcccgcactg ccgcagagcg tctgtgtatg acgaggttgt 300
25 tgtggagcgg cttttgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351
26 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly
27 1 5 10
29 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc 399
30 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu
31 15 20 25
33 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc 447
34 Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser
35 30 35 40
37 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt 495
38 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val
39 45 50 55
41 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat 543
42 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn
43 60 65 70 75
45 tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag 591
46 Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys
47 80 85 90
49 ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta 639
50 Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu
51 95 100 105

RAW SEQUENCE LISTING

DATE: 04/07/2006

PATENT APPLICATION: US/10/019,048A

TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

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53 tca gaa gta gca gta cac aac aag cca agc gat tgc tgg att gtt gta 687
54 Ser Glu Val Ala Val His Asn Lys Pro Ser Asp Cys Trp Ile Val Val
55      110      115      120
57 aaa aac aag gtg tat gat gtt tcc aat ttt gcg gac gag cat ccc gga 735
58 Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly
59      125      130      135
61 gga tca gtt att agt act tat ttt gga cga gac ggc aca gat gtt ttc 783
62 Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe
63 140      145      150      155
65 tct agt ttt cat gca gct tct aca tgg aaa att ctt caa gac ttt tac 831
66 Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr
67      160      165      170
69 att ggt gac gtg gag agg gtg gag ccg act cca gag ctg ctg aaa gat 879
70 Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp
71      175      180      185
73 ttc cga gaa atg aga gct ctt ttc ctg agg gag caa ctt ttc aaa agt 927
74 Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser
75      190      195      200
77 tcg aaa ttg tac tat gtt atg aag ctg ctc acg aat gtt gct att ttt 975
78 Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe
79      205      210      215
81 gct gcg agc att gca ata ata tgt tgg agc aag act att tca gcg gtt 1023
82 Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val
83 220      225      230      235
85 ttg gct tca gct tgt atg atg gct ctg tgt ttc caa cag tgc gga tgg 1071
86 Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp
87      240      245      250
89 cta tcc cat gat ttt ctc cac aat cag gtg ttt gag aca cgc tgg ctt 1119
90 Leu Ser His Asp Phe Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu
91      255      260      265
93 aat gaa gtt gtc ggg tat gtg atc ggc aac gcc gtt ctg ggg ttt agt 1167
94 Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser
95      270      275      280
97 aca ggg tgg tgg aag gag aag cat aac ctt cat cat gct gct cca aat 1215
98 Thr Gly Trp Trp Lys Glu Lys His Asn Leu His His Ala Ala Pro Asn
99      285      290      295
101 gaa tgc gat cag act tac caa cca att gat gaa gat att gat act ctc 1263
102 Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu
103 300      305      310      315
105 ccc ctc att gcc tgg agc aag gac ata ctg gcc aca gtt gag aat aag 1311
106 Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys
107      320      325      330
109 aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg 1359
110 Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu
111      335      340      345
113 tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg agc tgg aga tat acc 1407
114 Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr
115      350      355      360
117 tct aca gca gtg ctc tca cct gtc gac agg ttg ttg gag aag gga act 1455

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006

TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

118 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr
 119 365 370 375
 121 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc 1503
 122 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu
 123 380 385 390 395
 125 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc 1551
 126 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser
 127 400 405 410
 129 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag 1599
 130 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu
 131 415 420 425
 133 gtt tat aat tcg tct aaa gaa ttc gtg agt gca cag atc gta tcc aca 1647
 134 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr
 135 430 435 440
 137 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt 1695
 138 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu
 139 445 450 455
 141 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat 1743
 142 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
 143 460 465 470 475
 145 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt 1791
 146 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly
 147 480 485 490
 149 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg 1839
 150 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu
 151 495 500 505
 153 aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc 1887
 154 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Glu Gln His Ala Thr
 155 510 515 520
 157 acc agt taa cagtctttgg aaagcttggc aattgatctt tattctccac 1936
 158 Thr Ser
 159 525
 161 ggcagttgct tgtttgtttt ggggtgaatg accgaatgta ctggcatcca ttcttctgta 1996
 163 gccatcaatt ttgaac 2012
 272 <210> SEQ ID NO: 3
 273 <211> LENGTH: 6
 274 <212> TYPE: PRT
 275 <213> ORGANISM: Unknown
 W--> 277 <220> FEATURE:
 W--> 277 <223> OTHER INFORMATION: *see p.6 for error explanation*
 W--> 277 <400> 3
 278 Ser Glu Lys Asp Glu Leu
 E--> 279 *5* *misaligned amino acid numbering (see item 3 on Error Summary sheet)*
 281 <210> SEQ ID NO: 4
 282 <211> LENGTH: 20
 283 <212> TYPE: DNA
 284 <213> ORGANISM: Unknown
 W--> 286 <220> FEATURE: *same error*
 W--> 286 <223> OTHER INFORMATION:
see p.4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006

TIME: 10:25:46

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

W--> 286 <400> 4

E--> 287 tgggtggaart ggamfcayaa 20

352 <210> SEQ ID NO: 12

353 <211> LENGTH: 60

354 <212> TYPE: DNA

355 <213> ORGANISM: Unknown

W--> 357 <220> FEATURE:

W--> 357 <223> OTHER INFORMATION:

W--> 357 <400> 12

358 gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

W--> 371 HEINZ et al.

E--> 372 s.n. 10/019,048

E--> 373 notice to comply 03/28/2006

E--> 375 1

*invited nucleic acid designation**see p. 6**delete**see pp 7-8*

SEQUENCE LISTING

10/019,048A

5

<1107
<1207
<1307
<1407
<1417
<1607



Insert these
mandatory.

~~SEQUENCE LISTING~~

rename, identify and their responses

at beginning of sequence
listing

<170> PatentIn Vers. 3.3

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006
TIME: 10:25:47

Input Set : N:\SMITH\PTO.TS.14.txt
Output Set: N:\CRF4\04072006\J019048A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63
Seq#:1; Line(s) 64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83
Seq#:1; Line(s) 84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:1; Line(s) 103,104,105,106,107,108,109,110,111,112,113,114,115,116,117
Seq#:1; Line(s) 118,119,120,121,122,123,124,125,126,127,128,129,130,131,132
Seq#:1; Line(s) 133,134,135,136,137,138,139,140,141,142,143,144,145,146,147
Seq#:1; Line(s) 148,149,150,151,152,153,154,155,156,157,158,159,160,161,162
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Seq#:2; Line(s) 212,213,214,215,216,217,218,219,220,221,222,223,224,225,226
Seq#:2; Line(s) 227,228,229,230,231,232,233,234,235,236,237,238,239,240,241
Seq#:2; Line(s) 242,243,244,245,246,247,248,249,250,251,252,253,254,255,256
Seq#:2; Line(s) 257,258,259,260,261,262,263,264,265,266,267,268,269,270,271
Seq#:2; Line(s) 272
Seq#:3; Line(s) 274,277,281
Seq#:4; Line(s) 286,290
Seq#:5; Line(s) 295,299
Seq#:6; Line(s) 304,308
Seq#:7; Line(s) 313,317
Seq#:8; Line(s) 322,326
Seq#:9; Line(s) 331,335
Seq#:10; Line(s) 340,344
Seq#:11; Line(s) 349,352
Seq#:12; Line(s) 357

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:3,4,5,6,7,8,9,10,11,12

PatentIn 2.0 "bug":

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

10/019, 048A

7

<210> 5

<211> 17

<212> DNA

<213> Unknown

needs explanation - see p. 6

<400> 5

gggaanarrt grtgytc

17

see p. 8

8

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006

TIME: 10:25:47

FYI

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 6

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,048A

DATE: 04/07/2006

TIME: 10:25:47

Input Set : N:\SMITH\PTO.TS.14.txt

Output Set: N:\CRF4\04072006\J019048A.raw

L:3 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION NUMBER: is Added.

L:0 M:282 E: Numeric Field Identifier Missing, <160> is required.

L:0 M:282 E: Numeric Field Identifier Missing, <110> is required.

L:0 M:282 E: Numeric Field Identifier Missing, <120> is required.

L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213> ORGANISM:Unknown

L:277 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213> ORGANISM:Unknown

L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:277

L:279 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3

L:286 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213> ORGANISM:Unknown

L:286 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213> ORGANISM:Unknown

L:286 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:286

L:287 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:295 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213> ORGANISM:Unknown

L:295 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213> ORGANISM:Unknown

L:295 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:295

L:296 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5

L:296 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:304 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213> ORGANISM:Unknown

L:304 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213> ORGANISM:Unknown

L:304 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:304

L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213> ORGANISM:Unknown

L:313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213> ORGANISM:Unknown

L:313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:313

L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213> ORGANISM:Unknown

L:322 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213> ORGANISM:Unknown

L:322 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:322

L:331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213> ORGANISM:Unknown

L:331 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213> ORGANISM:Unknown

L:331 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:331

L:340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213> ORGANISM:Unknown

L:340 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213> ORGANISM:Unknown

L:340 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:340

L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213> ORGANISM:Unknown

L:349 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

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ORGANISM:Unknown

L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:349

L:357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>

ORGANISM:Unknown

L:357 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>

ORGANISM:Unknown

L:357 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:357

L:371 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3

L:372 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12

L:372 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12

L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:60

L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:372 M:254 E: No. of Bases conflict, LENGTH:Input:19 Counted:66 SEQ:12

L:372 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9

L:372 M:112 C: (48) String data converted to lower case,

M:341 Repeated in SeqNo=12

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M:254 Repeated in SeqNo=12

L:373 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13

M:112 Repeated in SeqNo=12

L:375 M:252 E: No. of Seq. differs, <211> LENGTH:Input:60 Found:82 SEQ:12

L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (12)